



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/641,319

Source: OIPE

Date Processed by STIC: 6-8-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1 825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/641,319

DATE: 06/08/2001
 TIME: 16:49:41

Input Set : A:\04578~1.txt
 Output Set: N:\CRF3\06082001\I641319.raw

3 <110> APPLICANT: Slater, Michael
 4 Huang, Fen
 5 Hartnett, James
 7 <120> TITLE OF INVENTION: Mutant TNE Polymerases
 9 <130> FILE REFERENCE: PRMG-04578
 11 <140> CURRENT APPLICATION NUMBER: 09/641,319

C--> 12 <141> CURRENT FILING DATE: 2001-05-08

14 <150> PRIOR APPLICATION NUMBER: 03/385,986

15 <151> PRIOR FILING DATE: 1993-08-30

17 <150> PRIOR APPLICATION NUMBER: 02/484,661

18 <151> PRIOR FILING DATE: 1995-06-17

20 <160> NUMBER OF SEQ ID NOS: 51

22 <170> SOFTWARE: PatentIn version 7.0

24 <180> SEQ ID NO: 1

25 <211> LENGTH: 2642

26 <212> TYPE: DNA

27 <213> ORGANISM: Thermotoga neapolitana

29 <220> FEATURE:

30 <221> NAME/KEY: CDS

31 <222> LOCATION: (1)..(3678)

33 <400> SEQUENCE: 1

34 tgc ggc aga cta ttt ctc ttt gat ggc aca gcc ctg gcc tac agg gca 48
 35 Met Ala Arg Leu Phe Leu Asp Gly Thr Ala Leu Ala Tyr Arg Ala

36 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

36 ttt tac gcc ctc gag aga tcc ttt ttt aca tcc aca gga att cca aac 36

37 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr

40 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

41 aac gcc gtc tat tgg gtt gtc agg atc ctc ttg aca ttc att aca aag gaa 144

42 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu

44 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

46 cac att ata ccc gaa aag gac tac tgg gtc gtc gac aag aag 132

47 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys

48 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

50 gca gcg aeg ttc tgg aca ctt gtt gaa ggg tac aag ggg caa agg 240

51 Ala Ala Thr Phe Arg His Lys Leu Lys Glu Ala Tyr Lys Ala Gln Arg

52 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

54 cca aag aeg cgg gat ctt cta gtt tgg gag cta cct tac atc aag cgg 288

55 Pro Lys Thr Pro Asp Leu Val Gln Lys Leu Pro Tyr Ile Lys Arg

56 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

57 ctg ata gaa gtt ctt ggt ttc aaa tgg ctg gag ctg gaa gga tac gaa 356

58 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu

60 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

62 gca gag gat atc atc gcc aeg ctt gtc mag ggc tac acg ttt ttt 384

63 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe

64 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 3678

66 gag gag att ttc ata atc acc ggt gtc aag gag atc ctt caa ctt gta 432

67 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val

Does Not Comply
 Corrected Diskette Needed

See p 6

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/641,319

DATE: 06/08/2001

TIME: 16:43:41

Input Set : A:\04578~1.txt

Output Set: N:\CRF3\06082001\I641319.raw

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135	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro	
136	405 410 415	
137	aac gag aaa aaa ttc aat ctc gaa gat ctg act ttg aaa ttt ctc gga	1296
138	Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly	
139	420 425 430	
140	tac aaa atg acg tct tat cag gaa ctg atg tcc ttt tcc tca cca ctt	1344
141	Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu	
142	435 440 445	
143	ttt ggt ttc agc ttt gcg gat gtt cgg gta gac aag gtt gcg gac tat	1392
144	Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr	
145	450 455 460	
146	tcc tgc gag gat gca gac atc act tat agg ctc tac aag ata atc ayt	1440
147	Ser Cys Glu Asp Ala Asp Ile Phe Tyr Arg Leu Tyr Lys Ile Leu Ser	
148	465 470 475 480	
149	atg aag ctc cat gaa ggg gaa ctt gag ttc ttc tac agg ata gag	1488
150	Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu	
151	485 490 495	
152	atg ccg ctt gtc aac gtt ctt gca ctc aat jaa ttt gac aag tgg ity tat	1536
153	Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr	
154	500 505 510	
155	gtg gac aca gaa ttc ctg aaa aag ctc tct gag gtc tac tgg taa aag	1584
156	Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys	
157	515 520 525	
158	ctc gag gaa ctg gtc gta aaa atc tac ttt atc gca gta gaa ccc ttc	1632
159	Leu Glu Glu Leu Ala Glu Ile Tyr Glu Ile Ala Gly Glu Pro Phe	
160	530 535 540	
161	aac atc aat tct cca aaa cag gtt tca aag atc ctt ttt gat aag ctg	1680
162	Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu	
163	545 550 555 560	
164	gga ata aaa cct ctt gja aaa acg aca aat aca gja ggg taa met acc	1723
165	Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr	
166	565 570 575	
167	agg ata gag gtg tgg gta gag aca ggg att gaa ctc ggg atu gta ctc	1776
168	Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro	
169	580 585 590	
170	ctc att ctc gag ttc aya aag atc cag aat ctg aat ttg acc ttc aya	1824
171	Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile	
172	595 600 605	
173	gac acc ctt ccg aaa ctt gtc aac ccc aat acc ggg aya att cat gta	1872
174	Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala	
175	610 615 620	
176	tct ttc cac cag aig ggt acc gcc act ggc agg ttg ayt ayc ayt gat	1920
177	Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp	
178	625 630 635 640	
179	cca aat ctt cag aat ctt ccg aca aag ayc gaa gag gja aaa gaa att	1968
180	Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile	
181	645 650 655	
182	aga aaa gca att gtc ccc cag gat cca gac tgg tgg atc gtc ayt gcg	2016

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Input Set : A:\04578~1.txt
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199 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 200 660 675 670
 202 gat tat tcc caa ata gaa ctc agg aac ctc gct cat ctc agt ggt gat 2064
 203 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 204 675 680 685
 206 gag aac ctt atg aag gca ttc gag tag ggc atc gat atg gac acc itg 2112
 207 Glu Asn Leu Val Lys Ala Phe Glu His Gly Ile Asp Val His Thr Leu
 208 690 695 700
 210 act gcc tcc tgg atc tac tcc gta tag cca gaa gaa atg aac gaa gaa 2160
 211 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Gln Gln
 212 705 710 715 720
 214 atg cga cgg gtt gaa aag atg atg aac ttc tct ata ata ttc atg 2208
 215 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr His Val
 216 725 730 735
 217 aca ccg tac ggt ctt tcc tgg aca ttt gga ata ccc gtt aac gaa gca 2256
 218 Thr Pro Tyr His Leu Ser Val Arg Leu Gly Ile Pro Val Lys His Ala
 219 740 745 750
 222 gaa aag atg att ata agg tat ttc tcc ctc tat cca aag atg cgg cgg atg 2304
 223 Glu Lys Met Ile Ile Ser Tyr Thr Leu Tyr Pro Lys Val Arg Ser
 224 755 760 765
 226 tac atc cag cag gtt gtt cpa gag paa aas gag aag ccc tcc gtc agg 2352
 227 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 228 770 775 780
 230 act ctc ttt ppa aga aaa aca gat att ccc cag ctc atg paa agg pcc 2400
 231 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gin Leu Met Ala Arg Asp
 232 785 790 795 800
 234 aag aac acc cag tcc gaa ccc paa aca atc gca ata aac acc ccc att 2448
 235 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
 236 805 810 815
 238 cag uga acg jtg pcc gat ata ata aia ttc gct atg ata pcc ata pcc 2496
 239 Gin Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
 240 820 825 830
 242 gag cag ctg aca aca aga aac atg aac tcc aga atg atc att gag ptt 2544
 243 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
 244 835 840 845
 246 cat gag jaa ccc gtc ttc gag ptt ccc gat gag gaa aia gaa gaa cta
 247 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
 248 850 855 860
 249 gtt gat atg gtg atg aac aca aat gtc gtc gtc tct ptt 2592
 250 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 251 865 870 875 880
 254 ctc ctt gag ptt gac ata agc atc gga aaa aac tgg tct tga 2632
 255 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Arg Trp Ser
 256 885 890
 259 -210- SEQ ID NO: 2
 260 -211- LENGTH: 893
 261 -212- TYPE: PRT
 262 -213- ORGANISM: Thermotoga neapolitana
 264 -2400- SEQUENCE: 2

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Input Set : A:\04578~1.txt

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266 Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 267 1 5 10 15
 270 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 271 20 25 30
 274 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Gln
 275 30 40 45
 278 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 279 50 55 60
 282 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gin Arg
 283 65 70 75 80
 286 Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 287 80 90 95
 289 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Gln Gln Tyr Gln
 291 100 105 110
 294 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gln Cys Thr Phe Phe
 295 115 120 125
 298 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gin Leu Val
 300 130 135 140
 302 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 303 145 150 155 160
 306 Glu Leu Tyr Asp Ser Lys Lys Val Lys Gln Arg Tyr Gly Val Gln Pro
 307 165 170 175
 310 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Gln Ile Asp Asn
 311 180 185 190
 314 Ile Pro Gly Val Thr Gly Ile Gly Gln Lys Thr Ala Val Gln Leu Leu
 315 195 200 205
 318 Gly Lys Tyr Arg Asn Leu Gln Asp Ile Leu Gln Ile Asn Arg Gln Leu
 319 210 215 220
 323 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Asp Gln Val Ala Ile
 324 225 230 235 240
 326 Leu Ser Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 327 245 250 255
 330 Asp Trp Gln Gln Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 331 260 265 270
 334 Pro Ile Leu Lys Gln Leu Gln Phe Ala Ser Ile Met Lys Gln Leu Gln
 335 275 280 285
 338 Leu Tyr Gln Gln Ala Glu Pro Thr Gly Tyr Gln Ile Val Lys Asp His
 339 290 295 300
 342 Lys Thr Phe Gln Asp Leu Ile Gln Ile Leu Lys Gln Val Pro Ser Phe
 343 305 310 315 320
 346 Ala Leu Asp Leu Gln Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 347 325 330 335
 350 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Asp Tyr Tyr Ile Pro
 351 340 345 350
 354 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 355 360 365
 358 Lys Leu Lys Gln Ile Leu Gln Asp Pro Ser Ser Lys Ile Val Gly Gln
 359 370 375 380
 362 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro

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p 6

<210> 3
<211> 44
<212> DNA
<213> Artificial/Unknown

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<223> Synthetic

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44

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<212> DNA
<213> Artificial/Unknown

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<221> misc_feature
<223> Synthetic

<400> 4
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Similar <213> response.
Artificial sequence and unknown
are separate regions. This
may occur only once, it is to
not be accompanied by
³⁷
<220>, <223> features.

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<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
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<400> 5
aggccagggc tgtgccatca aagagaaaata gtctcgcca

39

Review 10/10/03
The types of errors shown exist throughout the Sequence Listing. Please check
subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/641,319

DATE: 06/08/2001

TIME: 16:49:42

Input Set : A:\04578~1.txt

Output Set: N:\CRF3\06082001\I641319.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:493 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:507 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:511 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:535 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:549 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:553 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:559 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
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L:1697 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
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Input Set : A:\04578~1.txt

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